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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/785,738A

DATE: 09/12/2001
TIME: 17:11:46

Input Set : A:\198482.1.txt
Output Set: N:\CRF3\09122001\I785738A.raw

REVERSED

3 <110> APPLICANT: Sauter, Margret M
4 Lorbiecke, Rene
6 <120> TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
7 CONDITIONS
9 <130> FILE REFERENCE: 2283/201
11 <140> CURRENT APPLICATION NUMBER: 09/785,738A
12 <141> CURRENT FILING DATE: 2001-02-16
14 <150> PRIOR APPLICATION NUMBER: 60/183,572
15 <151> PRIOR FILING DATE: 2000-02-18
17 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 872
23 <212> TYPE: DNA
24 <213> ORGANISM: Rice
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (69)..(668)
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33 caatccac atg gag aac gaa ttc cag ga aag acg gag gtg ata gaa 110
34 Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu
35 1 5 10
37 gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac 158
38 Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
39 15 20 25 30
41 cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga 206
42 Arg Glu Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
43 35 40 45
45 gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254
46 Val Ile Ser Trp Arg Leu Asn Pro Asn Trp Glu Asn Cys Glu Asn
47 50 55 60
49 ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt 302
50 Leu Lys Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys
51 65 70 75
53 gat gtg tgc cca gag aag ctg cca aat tat gaa act aag atc aag agt 350
54 Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser
55 80 85 90
57 ttc ttt gaa gaa cac ctg cat acc gat gaa gaa ata cgc tat tgt ctt 398
58 Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu
59 95 100 105 110
62 gaa ggg agt gga tac ttt gat gtg aga gac caa aat gat cag tgg att 446
63 Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile
64 115 120 125
66 cgt ata gca ctg aag aaa gga ggc att gtt ctg cct gca ggg atg 494
67 Arg Ile Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
68 130 135 140

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70 tac cac cgc ttt acg ttg gac acc gac aac tat atc aag gca atg cga 542
 71 Tyr His Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
 72 145 150 155
 74 ctg ttt gtt ggc gat cct gtt tgg aca ccc tac aac cgt ccc cat gac 590
 75 Leu Phe Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp
 76 160 165 170
 78 cat ctt cct gca aga aag gag ttt ttg gct aaa ctt ctc aag tca gaa 638
 79 His Leu Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
 80 175 180 185 190
 82 ggt gaa aat caa gca gtt gaa ggc ttc tga gggtttgtt gggctcctgc 688
 83 Gly Glu Asn Gln Ala Val Glu Gly Phe
 W--> 84 195 200
 86 actgcggttc tatattcaac ctgaataaga ttttatcgat caatgtaaat ttagcacagt 748
 88 ggctatggtc gccactcacc aacttgaatg gaaagatatta atgatttttta ttaatttcta 808
 90 tgtatcaatc ggcataatgc atttccgaaa tttttttca ataaacagga gtcatgaagc 868
 92 tgaa 872
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 96 <211> LENGTH: 199
 97 <212> TYPE: PRT
 98 <213> ORGANISM: Rice
 100 <400> SEQUENCE: 2

101 Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu Ala Trp
 102 1 5 10 15
 103 Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His Arg Glu
 104 20 25 30
 105 Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly Val Ile
 106 35 40 45
 107 Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn Leu Lys
 108 50 55 60
 109 Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys Asp Val
 110 65 70 75 80
 111 Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser Phe Phe
 112 85 90 95
 113 Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
 114 100 105 110
 115 Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Ile
 116 115 120 125
 117 Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
 118 130 135 140
 119 Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
 120 145 150 155 160
 121 Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
 122 165 170 175
 123 Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu Gly Glu
 124 180 185 190
 125 Asn Gln Ala Val Glu Gly Phe
 126 195
 130 <210> SEQ ID NO: 3
 131 <211> LENGTH: 980

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132 <212> TYPE: DNA
 133 <213> ORGANISM: Rice
 135 <220> FEATURE:
 136 <221> NAME/KEY: CDS
 137 <222> LOCATION: (139)..(735)
 139 <400> SEQUENCE: 3
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 142 aggcttatccg gaatcgagg ggttcccaa taggaaagca actcaggact caggagcggc 120
 144 gtctgagagg tttcagag atg gag aac cag ttc cag gat ggc aag gag gag 171
 145 Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu
 146 1 5 10
 148 gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt 219
 149 Val Ile Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
 150 15 20 25
 152 cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca 267
 153 Pro His His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
 154 30 35 40
 156 gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat 315
 157 Glu Leu Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
 158 45 50 55
 160 gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg 363
 161 Asp Glu Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
 162 60 65 70 75
 164 gat att tgt gat gtg tgt cca gaa aag ctg cca aac tat gag gct aag 411
 165 Asp Ile Cys Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys
 166 80 85 90
 168 ctg aaa aat ttc ttt gaa gaa cac ttg cat act gat gaa gag ata cgc 459
 169 Leu Lys Asn Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg
 170 95 100 105
 172 tat tgt ctt gag gga agt gga tac ttc gat gtc agg gac caa aat gat 507
 173 Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp
 174 110 115 120
 176 cag tgg atc cgt gta gca gtg aag aaa ggg ggc atg att gtt ttg cct 555
 177 Gln Trp Ile Arg Val Ala Val Lys Lys Gly Met Ile Val Leu Pro
 178 125 130 135
 180 gcg gga atg tat cac cgc ttc aca ttg gac agt gac aac tac atc aag 603
 181 Ala Gly Met Tyr His Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys
 182 140 145 150 155
 184 gca atg cgg ctc ttt gtg gga gag cct gtc tgg acg ccg tac aac cgt 651
 185 Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg
 186 160 165 170
 188 ccc cat gac cat ctg cca gct aga aag gag tat gtc gaa aaa att atc 699
 189 Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile
 190 175 180 185
 192 aac agg ggt gga act caa gct gtc gaa gct cgt taa aggcatatca 745
 193 Asn Arg Gly Gly Thr Gln Ala Val Glu Ala Arg
 194 190 195
 196 agatgtgctt cctagttcggtgttctgtta cactctacag atactgaata aactgtgcta 805
 198 tcagctgttcaatgggctc ctaccgacat cttacatcat ttggcagtat 865

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200 cccgcttaaa atctccctga aaatacgcac gtcaccatgt cagagtgtt atataacaata 925
 202 atgacacttc agtccacagt cagcaaggga ctaatgacaa aaaaaaaaaaaa aaaaa 980
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 206 <211> LENGTH: 198
 207 <212> TYPE: PRT
 208 <213> ORGANISM: Rice
 210 <400> SEQUENCE: 4
 211 Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu Val Ile Glu Ala Trp
 212 1 5 10 15
 213 Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His Arg Glu
 214 20 25 30
 215 Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser Glu Leu Gly Ile Leu
 216 35 40 45
 217 Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn Asp Glu Asn Leu Lys
 218 50 55 60
 219 Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met Asp Ile Cys Asp Val
 220 65 70 75 80
 221 Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys Leu Lys Asn Phe Phe
 222 85 90 95
 223 Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
 224 100 105 110
 225 Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Val
 226 115 120 125
 227 Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
 228 130 135 140
 229 Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
 230 145 150 155 160
 231 Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
 232 165 170 175
 233 Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile Asn Arg Gly Gly Thr
 234 180 185 190
 235 Gln Ala Val Glu Ala Arg
 236 195
 240 <210> SEQ ID NO: 5
 241 <211> LENGTH: 774
 242 <212> TYPE: DNA
 243 <213> ORGANISM: Tomato
 245 <220> FEATURE:
 246 <221> NAME/KEY: CDS
 247 <222> LOCATION: (1)..(591)
 249 <400> SEQUENCE: 5
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 251 Ala Pro Asp Pro Arg Glu Asp Val Ile Gln Ala Trp Tyr Met Asp Asp
 252 1 5 10 15
 254 aac gat gag gac cag agg ctt cct cat cac cgt gag cca aag gaa ttt 96
 255 Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
 256 20 25 30
 258 gtg tct ctt gac aag ctg gct gaa ctt gga gtg ctc agc tgg aga ctt 144
 259 Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu

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260	35	40	45	
262	gat gct gac aat tat gag act gat gag gag ttg aag aaa att	cgg gaa	192	
263	Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu			
264	50	55	60	
266	gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa		240	
267	Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys			
268	65	70	75	80
270	cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg		288	
271	Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu			
272	85	90	95	
274	cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt		336	
275	His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe			
276	100	105	110	
278	gat gtc cgc gat gtg aat gag agc tgg att cgc gtc tgg gta aag aaa		384	
279	Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys			
280	115	120	125	
282	ggt gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt		432	
283	Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu			
284	130	135	140	
286	gat tca agc aac tac att aag gca atg cgt ctc ttt gtt ggt gac cca		480	
287	Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro			
288	145	150	155	160
290	att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa		528	
291	Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln			
292	165	170	175	
294	gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt		576	
295	Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val			
296	180	185	190	
298	aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt		631	
299	Asn Ala Ala Ala			
300	195			
302	aataaaatatt accatatggg ggcttgctg ttcttgatgt gtgccttact aagcatgttt		691	
304	aatgttgtat tggcacta aataaaatcac cccctatggg agattgattt ttttatatgca		751	
306	agtggaaattt attatgtat ttt		774	
309	<210> SEQ ID NO: 6			
310	<211> LENGTH: 196			
311	<212> TYPE: PRT			
312	<213> ORGANISM: Tomato			
314	<400> SEQUENCE: 6			
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316	1	5	10	15
317	Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe			
318	20	25	30	
319	Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu			
320	35	40	45	
321	Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu			
322	50	55	60	
323	Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys			
324	65	70	75	80

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding entry.

VERIFICATION SUMMARY

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L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:400 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:822 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:932 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:934 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17